RAW SEQUENCE LISTING

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Application Serial Number: 10/768,030
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RAW SEQUENCE LISTING DATE: 10/18/2004
PATENT APPLICATION: **US/10/768,030** TIME: 10:55:39

Input Set : **A:\2004-10-11 0760-0329P.ST25.txt**
Output Set: **N:\CRF4\10182004\J768030.raw**

<110> APPLICANT: Yasuhiko MUNAKATA et al.

<120> TITLE OF INVENTION: NOVEL HUMAN PARVOVIRUS B19 RECEPTOR AND USES THEREOF

<130> FILE REFERENCE: 0760-0329P

<140> CURRENT APPLICATION NUMBER: US 10/768,030

<141> CURRENT FILING DATE: 2004-02-02

<160> NUMBER OF SEQ ID NOS: 5

<170> SOFTWARE: PatentIn 3.2

<210> SEQ ID NO: 1

<211> LENGTH: 732

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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1               5                  10                  15
Gly Phe Thr Met Ser Asn Ser Ile Pro Gly Ile Glu Ser Pro Phe Glu
            20                  25                  30
Gln Ala Lys Lys Val Ile Thr Met Phe Val Gln Arg Gln Val Phe Ala
        35                  40                  45
Glu Asn Lys Asp Glu Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr
    50                  55                  60
Asp Asn Pro Leu Ser Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His
65                  70                  75                  80
Arg His Leu Met Leu Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Ser
                85                  90                  95
Lys Ile Gln Pro Gly Ser Gln Gln Ala Asp Phe Leu Asp Ala Leu Ile
            100                 105                 110
Val Ser Met Asp Val Ile Gln His Glu Thr Ile Gly Lys Lys Phe Glu
        115                 120                 125
Lys Arg His Ile Glu Ile Phe Thr Asp Leu Ser Ser Arg Phe Ser Lys
    130                 135                 140
Ser Gln Leu Asp Ile Ile Ile His Ser Leu Lys Lys Cys Asp Ile Ser
145                 150                 155                 160
Leu Gln Phe Phe Leu Pro Phe Ser Leu Gly Lys Glu Asp Gly Ser Gly
                165                 170                 175
Asp Arg Gly Asp Gly Pro Phe Arg Leu Gly Gly His Gly Pro Ser Phe
            180                 185                 190
Pro Leu Lys Gly Ile Thr Glu Gln Gln Lys Glu Gly Leu Glu Ile Val
        195                 200                 205
Lys Met Val Met Ile Ser Leu Glu Gly Glu Asp Gly Leu Asp Glu Ile
    210                 215                 220
Tyr Ser Phe Ser Glu Ser Leu Arg Lys Leu Cys Val Phe Lys Lys Ile
225                 230                 235                 240
Glu Arg His Ser Ile His Trp Pro Cys Arg Leu Thr Ile Gly Ser Asn
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53                  245                 250                 255
54 Leu Ser Ile Arg Ile Ala Ala Tyr Lys Ser Ile Leu Gln Glu Arg Val
55              260                 265                 270
56 Lys Lys Thr Trp Thr Val Val Asp Ala Lys Thr Leu Lys Lys Glu Asp
57          275                 280                 285
58 Ile Gln Lys Glu Thr Val Tyr Cys Leu Asn Asp Asp Asp Glu Thr Glu
59      290                 295                 300
60 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile
61 305                 310                 315                 320
62 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu
63                  325                 330                 335
64 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln
65              340                 345                 350
66 Arg Arg Phe Phe Met Gly Asn Gln Val Leu Lys Val Phe Ala Ala Arg
67          355                 360                 365
68 Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu
69      370                 375                 380
70 Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg
71 385                 390                 395                 400
72 Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr
73                  405                 410                 415
74 Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln
75              420                 425                 430
76 Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu
77          435                 440                 445
78 Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala
79      450                 455                 460
80 Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr
81 465                 470                 475                 480
82 Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His
83                  485                 490                 495
84 Arg Ala Leu His Pro Arg Glu Pro Leu Pro Pro Ile Gln Gln His Ile
85              500                 505                 510
86 Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile
87          515                 520                 525
88 Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys
89      530                 535                 540
90 Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp
91 545                 550                 555                 560
92 Gly Pro Thr Ala Lys Lys Leu Lys Thr Glu Gln Gly Gly Ala His Phe
93                  565                 570                 575
94 Ser Val Ser Ser Leu Ala Glu Gly Ser Val Thr Ser Val Gly Ser Val
95              580                 585                 590
96 Asn Pro Ala Glu Asn Phe Arg Val Leu Val Lys Gln Lys Lys Ala Ser
97          595                 600                 605
98 Phe Glu Glu Ala Ser Asn Gln Leu Ile Asn His Ile Glu Gln Phe Leu
99      610                 615                 620
100 Asp Thr Asn Glu Thr Pro Tyr Phe Met Lys Ser Ile Asp Cys Ile Arg
101 625                 630                 635                 640
```

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```
102 Ala Phe Arg Glu Glu Ala Ile Lys Phe Ser Glu Glu Gln Arg Phe Asn
103                 645                 650                 655
104 Asn Phe Leu Lys Ala Leu Gln Glu Lys Val Glu Ile Lys Gln Leu Asn
105             660                 665                 670
106 His Phe Trp Glu Ile Val Val Gln Asp Gly Ile Thr Leu Ile Thr Lys
107         675                 680                 685
108 Glu Glu Ala Ser Gly Ser Ser Val Thr Ala Glu Glu Ala Lys Lys Phe
109     690                 695                 700
110 Leu Ala Pro Lys Asp Lys Pro Ser Gly Asp Thr Ala Ala Val Phe Glu
111 705                 710                 715                 720
112 Glu Gly Gly Asp Val Asp Asp Leu Leu Asp Met Ile
113                 725                 730
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 3304
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 2
121 cgaccaaagc gcctgaggac cggcaac atg gtg cgg tcg ggg aat aag gca gct     54
122                             Met Val Arg Ser Gly Asn Lys Ala Ala
123                             1               5
125 gtt gtg ctg tgt atg gac gtg ggc ttt acc atg agt aac tcc att cct     102
126 Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser Asn Ser Ile Pro
127 10                  15                  20                  25
129 ggt ata gaa tcc cca ttt gaa caa gca aag aag gtg ata acc atg ttt     150
130 Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val Ile Thr Met Phe
131                 30                  35                  40
133 gta cag cga cag gtg ttt gct gag aac aag gat gag att gct tta gtc     198
134 Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu Ile Ala Leu Val
135             45                  50                  55
137 ctg ttt ggt aca gat ggc act gac aat ccc ctt tct ggt ggg gat cag     246
138 Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser Gly Gly Asp Gln
139         60                  65                  70
141 tat cag aac atc aca gtg cac aga cat ctg atg cta cca gat ttt gat     294
142 Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu Pro Asp Phe Asp
143     75                  80                  85
145 ttg ctg gag gac att gaa agc aaa atc caa cca ggt tct caa cag gct     342
146 Leu Leu Glu Asp Ile Glu Ser Lys Ile Gln Pro Gly Ser Gln Gln Ala
147 90                  95                  100                 105
149 gac ttc ctg gat gca cta atc gtg agc atg gat gtg att caa cat gaa     390
150 Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln His Glu
151                 110                 115                 120
153 aca ata gga aag aag ttt gag aag agg cat att gaa ata ttc act gac     438
154 Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe Thr Asp
155             125                 130                 135
157 ctc agc agc cga ttc agc aaa agt cag ctg gat att ata att cat agc     486
158 Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile His Ser
159         140                 145                 150
161 ttg aag aaa tgt gac atc tcc ctg caa ttc ttc ttg cct ttc tca ctt     534
162 Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe Ser Leu
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```
163     155                 160                 165
165 ggc aag gaa gat gga agt ggg gac aga gga gat ggc ccc ttt cgc tta      582
166 Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe Arg Leu
167 170                 175                 180                 185
169 ggt ggc cat ggg cct tcc ttt cca cta aaa gga att acc gaa cag caa      630
170 Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu Gln Gln
171                 190                 195                 200
173 aaa gaa ggt ctt gag ata gtg aaa atg gtg atg ata tct tta gaa ggt      678
174 Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu Gly
175             205                 210                 215
177 gaa gat ggg ttg gat gaa att tat tca ttc agt gag agt ctg aga aaa      726
178 Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg Lys
179         220                 225                 230
181 ctg tgc gtc ttc aag aaa att gag agg cat tcc att cac tgg ccc tgc      774
182 Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro Cys
183     235                 240                 245
185 cga ctg acc att ggc tcc aat ttg tct ata agg att gca gcc tat aaa      822
186 Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr Lys
187 250                 255                 260                 265
189 tcg att cta cag gag aga gtt aaa aag act tgg aca gtt gtg gat gca      870
190 Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp Ala
191                 270                 275                 280
193 aaa acc cta aaa aaa gaa gat ata caa aaa gaa aca gtt tat tgc tta      918
194 Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys Leu
195             285                 290                 295
197 aat gat gat gat gaa act gaa gtt tta aaa gag gat att att caa ggg      966
198 Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile Gln Gly
199         300                 305                 310
201 ttc cgc tat gga agt gat ata gtt cct ttc tct aaa gtg gat gag gaa     1014
202 Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu Glu
203     315                 320                 325
205 caa atg aaa tat aaa tcg gag ggg aag tgc ttc tct gtt ttg gga ttt     1062
206 Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly Phe
207 330                 335                 340                 345
209 tgt aaa tct tct cag gtt cag aga aga ttc ttc atg gga aat caa gtt     1110
210 Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln Val
211                 350                 355                 360
213 cta aag gtc ttt gca gca aga gat gat gag gca gct gca gtt gca ctt     1158
214 Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val Ala Leu
215             365                 370                 375
217 tcc tcc ctg att cat gct ttg gat gac tta gac atg gtg gcc ata gtt     1206
218 Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile Val
219         380                 385                 390
221 cga tat gct tat gac aaa aga gct aat cct caa gtc ggc gtg gct ttt     1254
222 Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala Phe
223     395                 400                 405
225 cct cat atc aag cat aac tat gag tgt tta gtg tat gtg cag ctg cct     1302
226 Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu Pro
227 410                 415                 420                 425
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```
229 ttc atg gaa gac ttg cgg caa tac atg ttt tca tcc ttg aaa aac agt     1350
230 Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn Ser
231                 430                 435                 440
233 aag aaa tat gct ccc acc gag gca cag ttg aat gct gtt gat gct ttg     1398
234 Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala Leu
235             445                 450                 455
237 att gac tcc atg agc ttg gca aag aaa gat gag aag aca gac acc ctt     1446
238 Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr Leu
239         460                 465                 470
241 gaa gac ttg ttt cca acc acc aaa atc cca aat cct cga ttt cag aga     1494
242 Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln Arg
243     475                 480                 485
245 tta ttt cag tgt ctg ctg cac aga gct tta cat ccc cgg gag cct cta     1542
246 Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro Leu
247 490                 495                 500                 505
249 ccc cca att cag cag cat att tgg aat atg ctg aat cct ccc gct gag     1590
250 Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro Ala Glu
251                 510                 515                 520
253 gtg aca aca aaa agt cag att cct ctc tct aaa ata aag acc ctt ttt     1638
254 Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu Phe
255             525                 530                 535
257 cct ctg att gaa gcc aag aaa aag gat caa gtg act gct cag gaa att     1686
258 Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln Glu Ile
259         540                 545                 550
261 ttc caa gac aac cat gaa gat gga cct aca gct aaa aaa tta aag act     1734
262 Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Lys Leu Lys Thr
263     555                 560                 565
265 gag caa ggg gga gcc cac ttc agc gtc tcc agt ctg gct gaa ggc agt     1782
266 Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly Ser
267 570                 575                 580                 585
269 gtc acc tct gtt gga agt gtg aat cct gct gaa aac ttc cgt gtt cta     1830
270 Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val Leu
271                 590                 595                 600
273 gtg aaa cag aag aag gcc agc ttt gag gaa gcg agt aac cag ctc ata     1878
274 Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu Ile
275             605                 610                 615
277 aat cac atc gaa cag ttt ttg gat act aat gaa aca ccg tat ttt atg     1926
278 Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe Met
279         620                 625                 630
281 aag agc ata gac tgc atc cga gcc ttc cgg gaa gaa gcc att aag ttt     1974
282 Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys Phe
283     635                 640                 645
285 tca gaa gag cag cgc ttt aac aac ttc ctg aaa gcc ctt caa gag aaa     2022
286 Ser Glu Glu Gln Arg Phe Asn Asn Phe Leu Lys Ala Leu Gln Glu Lys
287 650                 655                 660                 665
289 gtg gaa att aaa caa tta aat cat ttc tgg gaa att gtt gtc cag gat     2070
290 Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val Gln Asp
291                 670                 675                 680
293 gga att act ctg atc acc aaa gag gaa gcc tct gga agt tct gtc aca     2118
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